



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/820,790A

DATE: 07/30/2002

TIME: 14:20:53

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\07302002\I820790A.raw

4 <110> APPLICANT: SHAO, Wei et al.
 6 <120> TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 7 ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 8 THEREOF
 10 <130> FILE REFERENCE: CL001204
 12 <140> CURRENT APPLICATION NUMBER: 09/820,790A
 13 <141> CURRENT FILING DATE: 2001-03-30
 15 <160> NUMBER OF SEQ ID NOS: 4
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

618 <210> SEQ ID NO: 4
 619 <211> LENGTH: 542
 620 <212> TYPE: PRT
 621 <213> ORGANISM: Human
 623 <400> SEQUENCE: 4
 624 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
 625 1 5 10 15
 626 Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
 627 20 25 30
 628 Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
 629 35 40 45
 630 Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
 631 50 55 60
 632 Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
 633 65 70 75 80
 634 Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
 635 85 90 95
 636 Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
 637 100 105 110
 638 Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His
 639 115 120 125
 640 Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
 641 130 135 140
 642 Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu
 643 145 150 155 160
 644 Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly
 645 165 170 175
 646 Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly
 647 180 185 190
 648 Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu

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```

649          195          200          205
650 Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln
651          210          215          220
652 Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr
653 225          230          235          240
654 Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn
655          245          250          255
656 Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val
657          260          265          270
658 Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val
659          275          280          285
660 Glu Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile
661          290          295          300
662 Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Val Gly Arg Gln Thr
663 305          310          315          320
664 Thr Ala Pro Ala Thr Met Ser Thr Ala Ala Ser Gly Thr Thr Met Gly
665          325          330          335
666 Leu Val Glu Gln Ala Lys Ser Leu Leu Asn Lys Lys Ala Asp Gly Val
667          340          345          350
668 Lys Pro Gln Thr Asn Ser Thr Lys Asn Ser Ala Ala Ala Thr Ser Pro
669          355          360          365
670 Lys Gly Thr Leu Pro Pro Ala Al          Gln Thr Thr Val Ile
671          370          375
672 His Asn Pro Val Asp Gly Ile Lys Leu Ser          Ala Asn Thr
673 385          390          395
674 Thr Ile Glu Asp Glu Asp Ala Lys Ala Arg Lys Gln
675          405          410
676 Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala
677          420          430
678 Tyr Ala Lys Ile Cys Asn          Glu Pro Glu Ala
679          435
680 Leu Gly Asn Leu Val          u Gly Met Asp Phe His Al
681          450          455          460
682 Asn Leu Leu Al          Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn
683 465          470          475          480
684 Pro His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile
685          485          490
686 Arg Leu          Gln Tyr Ile Asp Gly Gln Gly Arg
687          500          505
688 Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn
689          515          520          525
690 Val His Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
691          530          535          540

```

E--> 696 (1)

VERIFICATION SUMMARY

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L:696 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4